OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/085,108

DATE: 03/13/2002
TIME: 10:18:02

Input Set : **N:\Crf3\RULE60\10085108.raw**
Output Set: **N:\CRF3\03132002\J085108.raw**

SEQUENCE LISTING

```
  1 (1) GENERAL INFORMATION:
  2        (i) APPLICANT: LUCAS, Sophie; BOON-FALLEUR, Thierry
  3       (ii) TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULES CODING
  4                                FOR
  5                                TUMOR REJECTION ANTIGEN PRECURSORS OF MEMBERS OF THE
MAGE-C AND
  6                                MAGE-B FAMILIES AND USES THEREOF
  7      (iii) NUMBER OF SEQUENCES: 26
  8       (iv) CORRESPONDENCE ADDRESS:
  9            (A) ADDRESSEE: Fulbright & Jaworski L.L.P.
 10            (B) STREET: 666 Fifth Avenue
 11            (C) CITY: New York City
 12            (D) STATE: New York
 13            (E) COUNTRY: USA
 14            (F) ZIP: 10103
 15        (v) COMPUTER READABLE FORM:
 16            (A) MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
 17            (B) COMPUTER: IBM PS/2
 18            (C) OPERATING SYSTEM: PC-DOS
 19            (D) SOFTWARE: Wordperfect
 20       (vi) CURRENT APPLICATION DATA:
C--> 21            (A) APPLICATION NUMBER: US/10/085,108
C--> 22            (B) FILING DATE: 01-Mar-2002
 23            (C) CLASSIFICATION:
 24      (vii) PRIOR APPLICATION DATA:
 25            (A) APPLICATION NUMBER: 09/501,104
 26            (B) FILING DATE: 09-Feb-2000
 27            (A) APPLICATION NUMBER: 09/468,433
 28            (B) FILING DATE: December 17, 1999
 29            (A) APPLICATION NUMBER: 09/066,281
 30            (B) FILING DATE: April 24, 1998
 31            (A) APPLICATION NUMBER: 08/845,528
 32            (B) FILING DATE: April 25, 1997
 33     (viii) ATTORNEY/AGENT INFORMATION:
 34            (A) NAME: Mary Anne Schofield
 35            (B) REGISTRATION NUMBER: 36,669
 36            (C) REFERENCE/DOCKET NUMBER: LUD 5611.1 JEL/MAS
 37       (ix) TELECOMMUNICATION INFORMATION:
 38            (A) TELEPHONE: (212) 318-3100
 39            (B) TELEFAX: (212) 318-3400
 40 (2) INFORMATION FOR SEQ ID NO: 1:
 41        (i) SEQUENCE CHARACTERISTICS:
 42            (A) LENGTH: 4031 base pairs
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ENTERED

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```
43            (B) TYPE: nucleic acid
44            (C) STRANDEDNESS: double-stranded
45            (D) TOPOLOGY: linear
46      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
47      GGATCGTCTC AGGTCAGCGG AGGGAGGAGA CTTATAGACC TATCCAGTCT TCAAGGTGCT 60
48      CCAGAAAGCA GGAGTTGAAG ACCTGGGTGT GAGGGACACA TACATCCTAA AAGCACCACA 120
49      GCAGAGGAGG CCCAGGCAGT GCCAGGAGTC AAGGTTCCCA GAAGACAAAC CCCCTAGGAA 180
50      GACAGGCGAC CTGTGAGGCC CTAGAGCACC ACCTTAAGAG AAGAAGAGCT GTAAGCCGGC 240
51      CTTTGTCAGA GCCATCATGG GGGACAAGGA TATGCCTACT GCTGGGATGC CGAGTCTTCT 300
52      CCAGAGTTCC TCTGAGAGTC CTCAGAGTTG TCCTGAGGGG GAGGACTCCC AGTCTCCTCT 360
53      CCAGATTCCC CAGAGTTCTC CTGAGAGCGA CGACACCCTG TATCCTCTCC AGAGTCCTCA 420
54      GAGTCGTTCT GAGGGGGAGG ACTCCTCGGA TCCTCTCCAG AGACCTCCTG AGGGGAAGGA 480
55      CTCCCAGTCT CCTCTCCAGA TTCCCCAGAG TTCTCCTGAG GGCGACGACA CCCAGTCTCC 540
56      TCTCCAGAAT TCTCAGAGTT CTCCTGAGGG GAAGGACTCC CTGTCTCCTC TAGAGATTTC 600
57      TCAGAGCCCT CCTGAGGGTG AGGATGTCCA GTCTCCTCTG CAGAATCCTG CGAGTTCCTT 660
58      CTTCTCCTCT GCTTTATTGA GTATTTTCCA GAGTTCCCCT GAGAGAACTC AGAGTACTTT 720
59      TGAGGGTTTT CCCCAGTCTC CTCTCCAGAT TCCTGTGAGC TCCTCCTCCT CCTCCACTTT 780
60      ATTGAGTCTT TTCCAGAGTT CCCCTGAGAG AACTCAGAGT ACTTTTGAGG GTTTTCCCCA 840
61      GTCTCTTCTC CAGATTCCTA TGACCTCCTC CTTCTCCTCT ACTTTATTGA GTATTTTCCA 900
62      GAGTTCTCCT GAGAGTGCTC AAAGTACTTT TGAGGGTTTT CCCCAGTCTC CTCTCCAGAT 960
63      TCCTGGGAGC CCCTCCTTCT CCTCCACTTT ACTGAGTCTT TTCCAGAGTT CCCCTGAGAG 1020
64      AACTCACAGT ACTTTTGAGG GTTTTCCCCA GTCTCCTCTC CAGATTCCTA TGACCTCCTC 1080
65      CTTCTCCTCT ACTTTATTGA GTATTTTCCA GAGTTCTCCT GAGAGTGCTC AAAGTACTTT 1140
66      TGAGGGTTTT CCCCAGTCTC CTCTCCAGAT TCCTGGGAGC CCCTCCTTCT CCTCCACTTT 1200
67      ACTGAGTCTT TTCCAGAGTT CCCCTGAGAG AACTCACAGT ACTTTTGAGG GTTTTCCCCA 1260
68      GTCTCCTCTC CAGATTCCTA TGACCTCCTC CTTCTCCTCT ACTTTATTGA GTATTTTACA 1320
69      GAGTTCTCCT GAGAGTGCTC AAAGTGCTTT TGAGGGTTTT CCCCAGTCTC CTCTCCAGAT 1380
70      TCCTGTGAGC TCCTCTTTCT CCTACACTTT ATTGAGTCTT TTCCAGAGTT CCCCTGAGAG 1440
71      AACTCAGAGT ACTTTTGAGG GTTTTCCCCA GTCTCCTCTC CAGATTCCTG TGAGCTCCTC 1500
72      CTCCTCCTCC TCCACTTTAT TGAGTCTTTT CCAGAGTTCC CCTGAGTGTA CTCAAAGTAC 1560
73      TTTTGAGGGT TTTCCCCAGT CTCCTCTCCA GATTCCTCAG AGTCCTCCTG AAGGGGAGAA 1620
74      TACCCATTCT CCTCTCCAGA TTGTTCCAAG TCTTCCTGAG TGGGAGGACT CCCTGTCTCC 1680
75      TCACTACTTT CCTCAGAGCC CTCCTCAGGG GGAGGACTCC CTATCTCCTC ACTACTTTCC 1740
76      TCAGAGCCCT CCTCAGGGGG AGGACTCCCT GTCTCCTCAC TACTTTCCTC AGAGCCCTCA 1800
77      GGGGGAGGAC TCCCTGTCTC CTCACTACTT TCCTCAGAGC CCTCCTCAGG GGGAGGACTC 1860
78      CATGTCTCCT CTCTACTTTC CTCAGAGTCC TCTTCAGGGG GAGGAATTCC AGTCTTCTCT 1920
79      CCAGAGCCCT GTGAGCATCT GCTCCTCCTC CACTCCATCC AGTCTTCCCC AGAGTTTCCC 1980
80      TGAGAGTTCT CAGAGTCCTC CTGAGGGGCC TGTCCAGTCT CCTCTCCATA GTCCTCAGAG 2040
81      CCCTCCTGAG GGGATGCACT CCCAATCTCC TCTCCAGAGT CCTGAGAGTG CTCCTGAGGG 2100
82      GGAGGATTCC CTGTCTCCTC TCCAAATTCC TCAGAGTCCT CTTGAGGGAG AGGACTCCCT 2160
83      GTCTTCTCTC CATTTTCCTC AGAGTCCTCC TGAGTGGGAG GACTCCCTCT CTCCTCTCCA 2220
84      CTTTCCTCAG TTTCCTCCTC AGGGGGAGGA CTTCCAGTCT TCTCTCCAGA GTCCTGTGAG 2280
85      TATCTGCTCC TCCTCCACTT CTTTGAGTCT TCCCCAGAGT TTCCCTGAGA GTCCTCAGAG 2340
86      TCCTCCTGAG GGCCTGCTC AGTCTCCTCT CCAGAGACCT GTCAGCTCCT TCTTCTCCTA 2400
87      CACTTTAGCG AGTCTTCTCC AAAGTTCCCA TGAGAGTCCT CAGAGTCCTC CTGAGGGGCC 2460
88      TGCCCAGTCT CCTCTCCAGA GTCCTGTGAG CTCCTTCCCC TCCTCCACTT CATCGAGTCT 2520
89      TTCCAGAGT TCTCCTGTGA GCTCCTTCCC CTCCTCCACT TCATCGAGTC TTTCCAAGAG 2580
90      TTCCCCTGAG AGTCCTCTCC AGAGTCCTGT GATCTCCTTC TCCTCCTCCA CTTCATTGAG 2640
91      CCCATTCAGT GAAGAGTCCA GCAGCCCAGT AGATGAATAT ACAAGTTCCT CAGACACCTT 2700
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```
 92        GCTAGAGAGT GATTCCTTGA CAGACAGCGA GTCCTTGATA GAGAGCGAGC CCTTGTTCAC 2760
 93        TTATACACTG GATGAAAAGG TGGACGAGTT GGCGCGGTTT CTTCTCCTCA AATATCAAGT 2820
 94        GAAGCAGCCT ATCACAAAGG CAGAGATGCT GACGAATGTC ATCAGCAGGT ACACGGGCTA 2880
 95        CTTTCCTGTG ATCTTCAGGA AAGCCCGTGA GTTCATAGAG ATACTTTTTG GCATTTCCCT 2940
 96        GAGAGAAGTG GACCCTGATG ACTCCTATGT CTTTGTAAAC ACATTAGACC TCACCTCTGA 3000
 97        GGGGTGTCTG AGTGATGAGC AGGGCATGTC CCAGAACCGC CTCCTGATTC TTATTCTGAG 3060
 98        TATCATCTTC ATAAAGGGCA CCTATGCCTC TGAGGAGGTC ATCTGGGATG TGCTGAGTGG 3120
 99        AATAGGGGTG CGTGCTGGGA GGGAGCACTT TGCCTTTGGG GAGCCCAGGG AGCTCCTCAC 3180
100        TAAAGTTTGG GTGCAGGAAC ATTACCTAGA GTACCGGGAG GTGCCCAACT CTTCTCCTCC 3240
101        TCGTTACGAA TTCCTGTGGG GTCCAAGAGC TCATTCAGAA GTCATTAAGA GGAAAGTAGT 3300
102        AGAGTTTTTG GCCATGCTAA AGAATACCGT CCCTATTACC TTTCCATCCT CTTACAAGGA 3360
103        TGCTTTGAAA GATGTGGAAG AGAGAGCCCA GGCCATAATT GACACCACAG ATGATTCGAC 3420
104        TGCCACAGAA AGTGCAAGCT CCAGTGTCAT GTCCCCCAGC TTCTCTTCTG AGTGAAGTCT 3480
105        AGGGCAGATT CTTCCCTCTG AGTTTGAAGG GGGCAGTCGA GTTTCTACGT GGTGGAGGGC 3540
106        CTGGTTGAGG CTGGAGAGAA CACAGTGCTA TTTGCATTTC TGTTCCATAT GGGTAGTTAT 3600
107        GGGGTTTACC TGTTTTACTT TTGGGTATTT TTCAAATGCT TTTCCTATTA ATAACAGGTT 3660
108        TAAATAGCTT CAGAATCCTA GTTTATGCAC ATGAGTCGCA CATGTATTGC TGTTTTTCTG 3720
109        GTTTAAGAGT AACAGTTTGA TATTTTGTAA AAACAAAAAC ACACCCAAAC ACACCACATT 3780
110        GGGAAAACCT TCTGCCTCAT TTTGTGATGT GTCACAGGTT AATGTGGTGT TACTGTAGGA 3840
111        ATTTTCTTGA AACTGTGAAG GAACTCTGCA GTTAAATAGT GGAATAAAGT AAAGGATTGT 3900
112        TAATGTTTGC ATTTCCTCAG GTCCTTTAGT CTGTTGTTCT TGAAAACTAA AGATACATAC 3960
113        CTGGTTTGCT TGGCTTACGT AAGAAAGTAG AAGAAAGTAA ACTGTAATAA ATAAAAAAAA 4020
114        AAAAAAAAAA A                                                      4031
```

116 (2) INFORMATION FOR SEQ ID NO: 2:
117   (i) SEQUENCE CHARACTERISTICS:
118   (A) LENGTH: 12 base pairs
119   (B) TYPE: nucleic acid
120   (C) STRANDEDNESS: single-stranded
121   (D) TOPOLOGY: linear
122   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
123   GATCTGCGGT GA   12
125 (2) INFORMATION FOR SEQ ID NO: 3:
126   (i) SEQUENCE CHARACTERISTICS:
127   (A) LENGTH: 12 base pairs
128   (B) TYPE: nucleic acid
129   (C) STRANDEDNESS: SINGLE-stranded
130   (D) TOPOLOGY: linear
131   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
132   GATCTGTTCA TG   12
134 (2) INFORMATION FOR SEQ ID NO: 4:
135   (i) SEQUENCE CHARACTERISTICS:
136   (A) LENGTH: 12 base pairs
137   (B) TYPE: nucleic acid
138   (C) STRANDEDNESS: single-stranded
139   (D) TOPOLOGY: linear
140   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
141   GATCTTCCCT CG   12
143 (2) INFORMATION FOR SEQ ID NO: 5:
144   (i) SEQUENCE CHARACTERISTICS:

RAW SEQUENCE LISTING   DATE: 03/13/2002
PATENT APPLICATION: US/10/085,108   TIME: 10:18:02

            Input Set : N:\Crf3\RULE60\10085108.raw
            Output Set: N:\CRF3\03132002\J085108.raw

```
145            (A) LENGTH: 46 base pairs
146            (B) TYPE: nucleic acid
147            (C) STRANDEDNESS: single-stranded
148            (D) TOPOLOGY: linear
149      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
150         NAACTGGAAG AATTCGCGGC CGCAGGAATT TTTTTTTTTT TTTTTT              46
152 (2) INFORMATION FOR SEQ ID NO: 6:
153         (i) SEQUENCE CHARACTERISTICS:
154            (A) LENGTH: 12 base pairs
155            (B) TYPE: nucleic acid
156            (C) STRANDEDNESS: single-stranded
157            (D) TOPOLOGY: linear
158      (ix) FEATURE:
159            (D) OTHER INFORMATION: BstX1 adapter upper strand
160      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
161         CTTTCCAGCA CA                                                   12
163 (2) INFORMATION FOR SEQ ID NO: 7:
164         (i) SEQUENCE CHARACTERISTICS:
165            (A) LENGTH: 1142 amino acids
166            (B) TYPE: amino acids
167            (C) STRANDEDNESS: single-stranded
168            (D) TOPOLOGY: linear
169      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
170         Met Gly Asp Lys Asp Met Pro Thr Ala Gly Met Pro Ser Leu Leu Gln
171                       5               10                  15
172         Ser Ser Ser Glu Ser Pro Gln Ser Cys Pro Glu Gly Glu Asp Ser Gln
173                      20               25                  30
174         Ser Pro Leu Gln Ile Pro Gln Ser Ser Pro Glu Ser Asp Asp Thr Leu
175                  35                   40                  45
176         Tyr Pro Leu Gln Ser Pro Gln Ser Arg Ser Glu Gly Glu Asp Ser Ser
177              50                   55                  60
178         Asp Pro Leu Gln Arg Pro Pro Glu Gly Lys Asp Ser Gln Ser Pro Leu
179         65                   70                  75                  80
180         Gln Ile Pro Gln Ser Ser Pro Glu Gly Asp Asp Thr Gln Ser Pro Leu
181                      85                   90                  95
182         Gln Asn Ser Gln Ser Ser Pro Glu Gly Lys Asp Ser Leu Ser Pro Leu
183                     100                  105                 110
184         Glu Ile Ser Gln Ser Pro Pro Glu Gly Glu Asp Val Gln Ser Pro Leu
185                     115                  120                 125
186         Gln Asn Pro Ala Ser Ser Phe Phe Ser Ser Ala Leu Leu Ser Ile Phe
187                     130                  135                 140
188         Gln Ser Ser Pro Glu Ser Ile Gln Ser Pro Phe Glu Gly Phe Pro Gln
189         145                  150                  155                 160
190         Ser Val Leu Gln Ile Pro Val Ser Ala Ala Ser Ser Ser Thr Leu Val
191                     165                  170                 175
192         Ser Ile Phe Gln Ser Ser Pro Glu Ser Thr Gln Ser Pro Phe Glu Gly
193                     180                  185                 190
194         Phe Pro Gln Ser Pro Leu Gln Ile Pro Val Ser Arg Ser Phe Ser Ser
195                  195                  200                  205
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196    Thr Leu Leu Ser Ile Phe Gln Ser Ser Pro Glu Arg Ser Gln Arg Thr
197        210             215             220
198    Ser Glu Gly Phe Ala Gln Ser Pro Leu Gln Ile Pro Val Ser Ser Ser
199    225             230             235                 240
200    Ser Ser Ser Thr Leu Leu Ser Leu Phe Gln Ser Ser Pro Glu Arg Thr
201            245             250                 255
202    Gln Ser Thr Phe Glu Gly Phe Pro Gln Ser Pro Leu Gln Ile Pro Val
203            260             265             270
204    Ser Arg Ser Phe Ser Ser Thr Leu Leu Ser Ile Phe Gln Ser Ser Pro
205        275.            280             285
206    Glu Arg Thr Gln Ser Thr Phe Glu Gly Phe Ala Gln Ser Pro Leu Gln
207        290             295             300
208    Ile Pro Val Ser Ser Ser Ser Ser Ser Thr Leu Leu Ser Leu Phe Gln
209    305             310             315                 320
210    Ser Ser Pro Glu Arg Thr Gln Ser Thr Phe Glu Gly Phe Pro Gln Ser
211            325             330             335
212    Leu Leu Gln Ile Pro Met Thr Ser Ser Phe Ser Ser Thr Leu Leu Ser
213            340             345             350
214    Ile Phe Gln Ser Ser Pro Glu Ser Ala Gln Ser Thr Phe Glu Gly Phe
215        355             360             365
216    Pro Gln Ser Pro Leu Gln Ile Pro Gly Ser Pro Ser Phe Ser Ser Thr
217        370             375             380
218    Leu Leu Ser Leu Phe Gln Ser Ser Pro Glu Arg Thr His Ser Thr Phe
219    385             390             395                 400
220    Glu Gly Phe Pro Gln Ser Pro Leu Gln Ile Pro Met Thr Ser Ser Phe
221            405             410             415
222    Ser Ser Thr Leu Leu Ser Ile Leu Gln Ser Ser Pro Glu Ser Ala Gln
223            420             425             430
224    Ser Ala Phe Glu Gly Phe Pro Gln Ser Pro Leu Gln Ile Pro Val Ser
225        435             440             445
226    Ser Ser Phe Ser Tyr Thr Leu Leu Ser Leu Phe Gln Ser Ser Pro Glu
227        450             455             460
228    Arg Thr Gln Ser Thr Phe Glu Gly Phe Pro Gln Ser Pro Leu Gln Ile
229    465             470             475                 480
230    Pro Val Ser Ser Ser Ser Ser Ser Ser Thr Leu Leu Ser Leu Phe Gln
231            485             490             495
232    Ser Ser Pro Glu Cys Thr Gln Ser Thr Phe Glu Gly Phe Pro Gln Ser
233            500             505             510
234    Pro Leu Gln Ile Pro Gln Ser Pro Pro Glu Gly Glu Asn Thr His Ser
235        515             520             525
236    Pro Leu Gln Ile Val Pro Ser Leu Pro Glu Trp Glu Asp Ser Leu Ser
237        530             535             540
238    Pro His Tyr Phe Pro Gln Ser Pro Gln Gly Glu Asp Ser Leu Ser
239    545             550             555                 560
240    Pro His Tyr Phe Pro Gln Ser Pro Pro Gln Gly Glu Asp Ser Leu Ser
241            565             570             575
242    Pro His Tyr Phe Pro Gln Ser Pro Gln Gly Glu Asp Ser Leu Ser Pro
243            580             585             590
244    His Tyr Phe Pro Gln Ser Pro Pro Gln Gly Glu Asp Ser Met Ser Pro
```

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 03/13/2002
PATENT APPLICATION: US/10/085,108   TIME: 10:18:03

Input Set : N:\Crf3\RULE60\10085108.raw
Output Set: N:\CRF3\03132002\J085108.raw

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 5

VERIFICATION SUMMARY   DATE: 03/13/2002
PATENT APPLICATION: US/10/085,108   TIME: 10:18:03

Input Set : N:\Crf3\RULE60\10085108.raw
Output Set: N:\CRF3\03132002\J085108.raw

L:21 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:22 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]